REMARKS

As a preliminary matter, Applicants's undersigned attorney directs the examiner's attention to the change of correspondence address included with this paper. Applicant's attorney requests that the change of address be made of record in connection with this application.

The Official Action dated April 10, 2002 and the references cited therein have been carefully reviewed. In view of the amendments presented herewith and the following remarks, favorable reconsideration and allowance of this application are respectfully requested.

Status of the claims and prosecution:

Claims 1-11, 13-17, 25 and 26 are pending. In the April 10, 2002 Official Action, all pending claims were rejected, and certain objections to the claims were made.

The previous rejection of claims 11-17 under 35 U.S.C. §112, first paragraph, as allegedly containing new matter, was withdrawn in light of Applicants' response in Paper No. 16, pointing to support for those amendments in the specification.

Claims 2, 3 and 11 were objected to because the word "nucleotide" in those claims is singular rather than plural.

Claims 1-11, 13-17, 25 and 26 remain rejected under 35 U.S.C. §112, first paragraph, for alleged lack of enablement. The examiner maintains that the specification, while being

enabling for a nucleic acid of SEQ ID NO:1 and bacterial and fungal cells transformed with that nucleic acid, does not reasonably provide enablement for allelic variants of SEQ ID NO:1 or its open reading frames or that hybridize to those nucleic acids. Specifically, in view of Farman et al. (2002), the examiner alleges that the specification provides no guidance on how to determine which allelic variants of SEQ ID NO:1 confer avirulence.

Claims 1-11, 13-17, 25 and 26 remain rejected under 35 U.S.C. §112, first paragraph, for alleged lack of adequate written description. The examiner alleges that the specification does not describe structural features that distinguish AVR-CO39 homologs that confer avirulence from those that do not.

Claims 1-3, 5, 8, 9, 11, 15, 16, 25 and 26 are rejected under 35 U.S.C. §112, second paragraph, for alleged indefiniteness on the following grounds: (1) claims 1, 11 and 25 are allegedly indefinite for failing to recite hybridization and wash times; (2) claims 2, 3 and 11 allegedly are not in proper Markush format; (3) claims 6 and 13 are allegedly confusing as to whether the recombinant DNA comprises the vector or whether the vector comprises the recombinant DNA; (4) claims 11 and 26 are allegedly indefinite in their recitation of "allelic variant"; and (5) claims 8, 9, 15 and 16 allegedly lack antecedent basis for the limitation "The cell" in line 1.

Claims 11 and 13-16 are rejected under 35 U.S.C. §102(b) as allegedly anticipated by either Sweigard et al. (1995, Plant Cell 7: 1221-1233) or Shimizu et al. (1991, Infect. Immunol. 59: 137-142). The examiner states that, since the claims do not recite hybridization

and wash times, the hybridization conditions set forth in the claims fail to distinguish the claimed sequences from those disclosed by either Sweigard et al. or Shimizu et al.

Claims 1-10, 17, 25 and 26 are deemed free of the prior art.

In accordance with the present amendment, claims 8, 10, 15 and 17 have been canceled, and claims 1-4, 6, 7, 9, 11, 13, 14, 16, 25 and 26 have been amended.

Claim 1 has been amended to call for an isolated nucleic acid molecule from *Magnaporthe grisea* strain 2539 comprising a segment of chromosome 1 approximately 1 kb in size and containing at least one open reading frame, the segment conferring rice cultivar CO39-specific avirulence to fungal plant pathogens that contain the nucleic acid, wherein the nucleic acid molecule hybridizes with SEQ ID NO:1 or its complement under specified hybridization and washing conditions that include buffer components, temperatures and times. Claims 2 and 3 now call for the portion of the nucleic acid molecule of claim 1 that is an open reading frame located between nucleotides 582 and 850 (ORF 3), or that hybridizes with that portion under hybridization conditions that further comprise a final washing in 0.1X SSC, 0.1% SDS at 65°C for 15 minutes. Claim 4 now specifies the nucleic acid molecule of claim 1 that encodes a polypeptide having the features of a polypeptide comprising SEQ ID NO:4. Claims 6, 7 and 9 have been amended to recite vectors comprising the nucleic acid molecule of claim 1, and fungal or bacterial cells transformed with those vectors.

Claim 11 as amended now calls for an isolated nucleic acid molecule having a sequence selected from the group consisting of: (a) SEQ ID NO:1; (b) a segment of SEQ ID NO: 1 comprising an open reading frame located between nucleotides 582 and 850; (c) a

sequence that hybridizes with the sequence of a) or b) or its complement under conditions comprising hybridization for 16 hours at 42°C in 5X SSC, 5X Denhardt's reagent, 7% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.125M NaHPO4, 50% formamide and 1 mM EDTA, rinsing with 2X SSC at room temperature, and washing once for 10 minutes and once for 15 minutes at 65°C in 2X SSC, followed by 15 minutes at 65°C in 0.1X SSC and 0.1% SDS; and (d) a sequence encoding a polypeptide having an amino acid sequence comprising SEQ ID NO:4. Claims 13, 14 and 16 have been amended to recite vectors comprising the nucleic acid molecule of claim 11, and fungal or bacterial cells transformed with those vectors.

Claim 25 has been amended to call for a transgenic epiphytic bacterium that expresses a portion of an isolated nucleic acid molecule from *Magnaporthe grisea* strain 2539 comprising a segment of chromosome 1 approximately 1 kb in size and containing at least one open reading frame, the segment conferring rice cultivar CO39-specific avirulence to fungal plant pathogens that contain the nucleic acid, wherein the nucleic acid molecule hybridizes with SEQ ID NO:1 or its complement under specified hybridization and washing conditions that include buffer components, temperatures and times. Claim 26 further specifies that the bacterium expresses the amino acid sequences of SEQ ID NO:2 or SEQ ID NO:4.

Applicants assert that the foregoing claim amendments overcome each of the objections and rejections issued in the April 10, 2002 Official Action, and that the claims as amended are in condition for allowance. Support for Applicants' assertion to this effect is set forth below.

Objection to the claims:

Claims 2, 3 and 11 were objected to because the word "nucleotide" in portions of those claims was singular rather than plural. The claims as amended no longer contain the objected-to recitations; accordingly, the objection should be withdrawn.

Rejections under 35 U.S.C. §112, first paragraph:

All claims stand rejected under 35 U.S.C. §112, first paragraph, for alleged lack of enablement and adequate written description. The examiner asserts that the specification, while being enabling for a nucleic acid of SEQ ID NO:1 and bacterial and fungal cells transformed with that nucleic acid, does not reasonably provide enablement for allelic variants of SEQ ID NO:1 or its open reading frames or that hybridize to those nucleic acids. Specifically, in view of Farman et al. (2002), the examiner alleges that the specification provides no guidance on how to determine which allelic variants of SEQ ID NO:1 confer avirulence. Furthermore, in support of the rejection for lack of adequate written description the examiner alleges that the specification does not describe structural features that distinguish AVR-CO39 homologs that confer avirulence from those that do not. Applicants traverse these rejections as applied to the claims as presently amended.

Turning first to claims 1-7, 9, 25 and 26, claim 1 has been amended to now specify that the nucleic acid molecule that confers cultivar-specific avirulence is isolated from *M. grisea* strain 2539 and hybridizes with SEQ ID NO:1 under specific hybridization and washing conditions. Inasmuch as the specification's working examples relate to a segment

isolated from strain 2539, it is clear that the specification more than adequately describes, and fully enables practice of the invention as claimed in claims 1-7 and 9. Likewise, claims 25 and 26, which have been similarly amended, are more than adequately described and fully enabled by the specification.

Turning next to claims 11, 13, 14 and 16, these claims are now limited to isolated nucleic acid molecules that, by virtue of the specific hybridization conditions now recited, are greater than 95% homologous to SEQ ID NO:1 or the portion thereof comprising ORF 3 and encoding SEQ ID NO:2. It should be noted that these claims do not contain the functional limitation that the recited sequences confer cultivar-specific avirulence (though they may). The utility of these sequences as stated at page 16-17 of the specification includes their use as probes to detect the presence and/or expression of *AVRI-CO39* genes and to identify homologs from other *Magnaporthe* isolates, as well as to produce quantities of substantially pure AVR1-CO39-encoded proteins. The specification more than adequately describes isolated nucleic acids with this level of homology to SEQ ID NO:1 or the ORF 3 portion thereof, and fully enables practice of the invention claimed in claims 11, 13, 14 and 16.

For the foregoing reasons, Applicants submit that the presently amended claims fully satisfy the written description and enablement requirements of the statute. Applicants therefore request withdrawal of the rejections under 35 U.S.C. §112, first paragraph.

Rejections under 35 U.S.C. §112, second paragraph:

Claims 1-3, 5, 8, 9, 11, 15, 16, 25 and 26 were rejected under 35 U.S.C. §112, second paragraph, for alleged indefiniteness on the several grounds. First, claims 1, 11 and 25 are allegedly indefinite for failing to recite hybridization and wash times. These claims have been amended to recite wash times. Accordingly, the rejection on this ground should be overcome.

Second, claims 2, 3 and 11 allegedly were not in proper Markush format. These claims have been amended to either (1) no longer contain a Markush group or (2) recite a Markush group in proper format. Hence, the rejection on this ground should be overcome.

Third, claims 6 - 13 were allegedly confusing as to whether the recombinant DNA comprises the vector or whether the vector comprises the recombinant DNA. The claims have been amended to recite a vector comprising the nucleic acid molecule of claim 1 or 11, and therefore no longer contain the allegedly confusing phrase.

Fourth, claims 11 and 26 were allegedly indefinite in their recitation of "allelic variant." These claims as amended no longer recite "allelic variant." Accordingly, the rejection on this ground should be overcome.

Finally, claims 8, 9, 15 and 16 allegedly lack antecedent basis for the limitation "The cell" in line 1. Claims 8 and 15 have been canceled. Claims 9 and 16 have been amended to recite "fungal or bacterial" cell, which has proper antecedent basis in the claims from which claims 9 and 16 depend. Hence, the rejection on this ground should be overcome.

In view of the foregoing claim amendments, Applicants submit that the rejections under 35 U.S.C. §112, second paragraph, should be withdrawn.

Rejections under 35 U.S.C. §102(b):

Claims 11 and 13-16 remain rejected or are newly rejected under 35 U.S.C. §102(b) as allegedly anticipated by Sweigard et al. (1995) or Shimizu et al. (1991). The examiner asserts that the cited references still anticipate the rejected claims because the recited hybridization conditions do not specify hybridization or wash times, so that the conditions lack sufficient stringency to distinguish the claimed sequences over those set forth in the cited references.

Claim 11 has now been amended to specify the hybridization and washing times referred in the specification at page 23, lines 16-33. The hybridization conditions now recited in claim 11 are sufficiently stringent that a hybrid of less than 95% homology would not be maintained. Applicants assert that none of the sequences of Sweigard et al. or Shimizu et al. is identical to the sequences recited in claim 11, in view of the hybridization conditions set forth in the claims. Accordingly, the rejection of claims 11 and 13-16 under 35 U.S.C. §102(b) based on Sweigard et al. or Shimizu et al. should be withdrawn.

Conclusion:

In view of the claim amendments submitted herewith and the foregoing remarks, the presently-pending claims are believed to be in condition for allowance. Applicants

respectfully request early and favorable reconsideration and withdrawal of the objections and rejections set forth in the April 10, 2002 Official Action, and allowance of this application.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "**Version with markings to show changes made.**"

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

1. (Three times amended) An isolated nucleic acid molecule from *Magnaporthe grisea* strain 2539 comprising a segment of chromosome 1 approximately 1 kb in size and containing at least one open reading frame, the segment conferring rice cultivar CO39-specific avirulence to fungal plant pathogens that contain the nucleic acid, wherein the nucleic acid molecule hybridizes with SEQ ID NO:1 or its complement under hybridization conditions comprising hybridization for at least 6 hours at 42°C in 5X SSC, 5X Denhardt's reagent, 1.0% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.05% sodium pyrophosphate and 50% formamide and washing conditions comprising 5 minutes at room temperature in 2X SSC and 1% SDS, followed by 15 minutes at room temperature in 2X SSC and 0.1% SDS; followed by 30 minutes to 1 hour at 37°C in 2X SSC and 0.1% SDS, followed by 2 hours at 55°C in 2X SSC and 0.1% SDS.

2. (Three times amended) The nucleic acid molecule of claim 1, having a nucleotide sequence that hybridizes with a portion of SEQ ID NO:1 or its complement, wherein the portion is [selected from the group consisting of :

an open reading frame located between nucleotide 358 and 495;

an open reading frame located between nucleotide 443 and 676;]

an open reading frame located between nucleotides 582 and 850[;

an open reading frame located between nucleotides 753 and 858;

an open reading frame located between nucleotides 885 and 1047;

an open reading frame on the complementary strand of SEQ ID NO:1 located between nucleotides 757 and 561;

an open reading frame on the complementary strand of SEQ ID NO: 1 located between nucleotides 419 and 312;],

wherein the hybridization conditions further comprise a final washing in 0.1X SSC, 0.1% SDS at 65°C for 15 minutes.

3. (Twice amended) The nucleic acid molecule of claim 2, comprising a portion of SEQ ID NO:1, wherein the portion is [selected from the group consisting of :

an open reading frame located between nucleotide 358 and 495;

an open reading frame located between nucleotide 443 and 676;]

an open reading frame located between nucleotides 582 and 850[;

an open reading frame located between nucleotides 753 and 858;

an open reading frame located between nucleotides 885 and 1047;

an open reading frame on the complementary strand of SEQ ID NO:1 located between nucleotides 757 and 561;

an open reading frame on the complementary strand of SEQ ID NO: 1 located between nucleotides 419 and 312].

4. (Amended) The nucleic acid molecule of claim 1, which encodes a polypeptide having the features of a polypeptide comprising [a sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3,] SEQ ID NO:4[, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8].

6. (Twice amended)A vector for transforming cells, [recombinant DNA molecule] comprising the nucleic acid molecule of claim 1[, inserted into a vector for transforming cells].

7. (Three times amended) A fungal[,] or bacterial, or plant] cell transformed with the vector [recombinant DNA molecule] of claim 6.

Cancel claim 8.

9. (Twice amended) The fungal or bacterial cell of claim 7, which is an epiphytic bacterial cell.

Cancel claim 10.

11. (Twice amended) An isolated nucleic acid molecule having a sequence selected from the group consisting of:

a) SEQ ID NO:1;

b) [an allelic variant of an isolated nucleic acid comprising SEQ ID NO:1;

c)] a segment of SEQ ID NO: 1 comprising [selected from the group consisting of:

an open reading frame located between nucleotide 358 and 495;

an open reading frame located between nucleotide 443 and 676;]

an open reading frame located between nucleotides 582 and 850;

[an open reading frame located between nucleotides 753 and 858;

an open reading frame located between nucleotides 885 and 1047;

an open reading frame on the complementary strand of SEQ ID NO:1 located between nucleotides 757 and 561;

an open reading frame on the complementary strand of SEQ ID NO: 1 located between nucleotides 419 and 312;

d) an allelic variant of the segment of SEQ ID NO:1;]

c [e]) a sequence that hybridizes with [any of] the sequence[s] of a) or b) [- d)] or its complement under conditions comprising hybridization for 16 hours at 42°C in 5X SSC, 5X Denhardt's reagent, 7% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.125M NaHPO4, 50% formamide and 1 mM EDTA, rinsing with 2X SSC at room temperature, and washing once for 10 minutes and once for 15 minutes at 65°C in 2X SSC, followed by 15 minutes at 65°C in 0.1X SSC and 0.1% SDS; and

f) a sequence encoding a polypeptide having an amino acid sequence comprising [any one of SEQ ID NO:2, SEQ ID NO:3,] SEQ ID NO:4[, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8].

13. (Twice amended) A vector for transforming cells, [recombinant DNA molecule] comprising the nucleic acid molecule of claim 11[, inserted into a vector for transforming cells].

14. (Three times amended) A fungal or bacterial[, fungal, or plant] cell transformed with the vector [recombinant DNA molecule] of claim 13.

Cancel claim 15.

16. (Twice amended) The fungal or bacterial cell of claim 14, which is an epiphytic bacterial cell.

Cancel claim 17.

25. (Twice amended) A transgenic epiphytic bacterium that expresses a portion of an isolated nucleic acid molecule from *Magnaporthe grisea* strain 2539 comprising a segment of chromosome 1 approximately 1 kb in size and containing at least one open reading frame, the

segment conferring rice cultivar CO39-specific avirulence to fungal plant pathogens that contain the nucleic acid, wherein the nucleic acid molecule hybridizes with SEQ ID NO:1 or its complement under hybridization conditions comprising hybridization for at least 6 hours at 42°C in 5X SSC, 5X Denhardt's reagent, 1.0% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.05% sodium pyrophosphate and 50% formamide and washing conditions comprising 5 minutes at room temperature in 2X SSC and 1% SDS, followed by 15 minutes at room temperature in 2X SSC and 0.1% SDS; followed by 30 minutes to 1 hour at 37°C in 2X SSC and 0.1% SDS, followed by 2 hours at 55°C in 2X SSC and 0.1% SDS.

26. (Three times amended) The transgenic epiphytic bacterium of claim 24, which expresses the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4[, or an allelic variant thereof].